

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/589,233
Source: TFWJP
Date Processed by STIC: 8/22/06

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 08/22/2006

PATENT APPLICATION: US/10/589,233

TIME: 14:21:39

Input Set : A:\STERN29.002APC SEQLIST.TXT
 Output Set: N:\CRF4\08222006\J589233.raw

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4 <110> APPLICANT: Giannotta, Fabrizio
5     Filee, Patrice
6     Galleni, Moreno
7     Frere, Jean-Marie
8     Joris, Bernard
9     Brans, Alain
10    Ruth, Nadia
12 <120> TITLE OF INVENTION: HYBRID PROTEINS OF ACTIVE-SITE SERINE
13    BETA-LACTAMASE
15 <130> FILE REFERENCE: STERN29.002APC
C--> 17 <140> CURRENT APPLICATION NUMBER: US/10/589,233
C--> 17 <141> CURRENT FILING DATE: 2006-08-10
17 <150> PRIOR APPLICATION NUMBER: PCT/EP2005/050174
18 <151> PRIOR FILING DATE: 2005-01-17
20 <150> PRIOR APPLICATION NUMBER: EP 04075430.1
21 <151> PRIOR FILING DATE: 2001-02-11
23 <160> NUMBER OF SEQ ID NOS: 68
25 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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28 <211> LENGTH: 858
29 <212> TYPE: DNA
30 <213> ORGANISM: Escherichia coli
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35 tgctgcaatg ataccgcgag acccacgctc accggctcca gatttatcag caataaaacca 180
36 gccagccgga agggccgagc gcagaagtgg tcctgcaact ttatccgcct ccatccagtc 240
37 tattaattgt tgccgggaag ctagagtaag tagttcgcca gttaatagtt tgcccaacgt 300
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42 gactggtgag tactcaacca agtcattctg agaatagtgt atgcggcgcac cgagttgctc 600
43 ttgccccggc tcaacacggg ataataccgc gccacatagc agaactttaa aagtgcctat 660
44 catggaaaaa cgttctcgg ggcgaaaaact ctcaaggatc ttaccgctgt tgagatccag 720
45 ttcgatgtaa cccactcggt cacccaaactg atcttcagca tcttttactt tcaccagcgt 780
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47 gaaatgttga atactcat                                         858
49 <210> SEQ ID NO: 2
50 <211> LENGTH: 921
51 <212> TYPE: DNA
52 <213> ORGANISM: Bacillus licheniformis
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55 atgaaaattat ggttcagttac tttaaaaactg aaaaaggctg cagcagtgtt gctttctct 60
 56 tgcgtcgccg ttgcaggatg cgctaacaat caaacaatg cctcgcaacc tgccgagaag 120
 57 aatgaaaaga cggagatgaa agatgatttt gaaaaacttg aggaacaatt tgatcaaaa 180
 58 ctcgggatct ttgcatttgg aacccggacgg tagcgtatcg gccggatgag 240
 59 cgtttgctt ttgcttcgac gattaaggct ttaactgttag gcgtgcttt gcaacagaaaa 300
 60 tcaatagaag atctgaacca gagaataaca tatacacgtg atgatcttgt aaactacaac 360
 61 ccgattacgg aaaagcacgt tgatacggga atgacgctca aagagcttcg ggtatgctcg 420
 62 cttcgatata gtgacaatgc ggcacagaat ctcatctta aacaaattgg cggacactgaa 480
 63 agtttggaaaa aggaactgag gaagattggat gatgaggatca aacatcccgaa acgattcgaa 540
 64 ccagagttaa atgaagtgaa tccgggtgaa actcaggata ccagtacagc aagagcactt 600
 65 gtcacaagcc ttgcggccctt tgctcttgaa gataaaacttc caagtggaaa acgcgagctt 660
 66 ttaatcgatt ggatgaaacg aaataaccact ggagacgcct taatccgtgc cgggtgtccg 720
 67 gacgggttggg aagtggctga taaaactgga gccggcatcat atggaaccccg gaatgacatt 780
 68 gccatcattt ggccgcacaa aggagatcct gtcgtcttg cagtattatc cagcaggat 840
 69 aaaaaggacg ccaagtatga tgataaaactt attgcagagg caacaaaggt ggtaatgaaa 900
 70 gccttaaaca tgaacggcaa a 921
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 74 <212> TYPE: DNA
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 79 ccgctgggtgg cctgcgtca ggcgtcgggc tccgagagcg gccagcagcc cggctcgcc 120
 80 gtttgcggga cgagcgcaca cgctcgccgg gacgcccacg agaaggaggat cggggcgctg 180
 81 gagaagaagt tcgacgcccc ccctggcgctc tacgccccatcg acaccccgca cggccaggag 240
 82 atcaccaccggc gggccgacga gcgcgttcgca tacggctcga cttcaaggc cttccaggcg 300
 83 ggcgcgatcc ttgcgcaagt tctccgagac gggcgcgaag tccggcgggg cggcgaggcc 360
 84 gacggcatgg acaagggtggt ccactacggg caggacgcga tcctgccccaa ctacccggtg 420
 85 accgagaagc acgtcgccga cggcatgtcc ctgcgcgagc tgcgtcgacgc cgtcggtggcc 480
 86 tacagcgaca acaccgcggc caacctgtctc ttgcaccagc tcggcgccgg aaggggctca 540
 87 acgcgggtcc tcaagcgact cggcgaccac accacgagca tggaccgcta cgagcaggag 600
 88 ctgggctcggtt ccgtccccgg cgaccccccgg gacaccagca cggccgcgcgc gttcgccgag 660
 89 gacctgcgcg ctttcgcccgt cgaggacggc gagaaggccg ccctcgccgc caacgaccgc 720
 90 gagcagctga acgactggat gagcggggagc aggaccggcg acgcgtatcg ccggggccgt 780
 91 gtgccgaagg actggaaaggat ggaggacaag agcggccagg tcaagtacgg caccggAAC 840
 92 gacatcgccg tcgtccggcc gccggggccgc gccggatcg tcgtctcggt gatgagccac 900
 93 ggcgacaccc aggacggcga gccgcacgac gagctggtgg ccgaggccgg ctcgtcgctc 960
 94 gccgacggtc tgaag 975
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 97 <211> LENGTH: 286
 98 <212> TYPE: PRT
 99 <213> ORGANISM: Escherichia coli
 101 <400> SEQUENCE: 4
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 103 1 5 10 15
 104 Phe Cys Leu Pro Val Phe Ala His Pro Glu Thr Leu Val Lys Val Lys
 105 20 25 30
 106 Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp
 107 35 40 45

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108 Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe
 109 50 55 60
 110 Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser
 111 65 70 75 80
 112 Arg Val Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser
 113 85 90 95
 114 Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His Leu Thr
 115 100 105 110
 116 Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser
 117 115 120 125
 118 Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys
 119 130 135 140
 120 Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp His Val Thr Arg Leu
 121 145 150 155 160
 122 Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg
 123 165 170 175
 124 Asp Thr Thr Met Pro Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu
 125 180 185 190
 126 Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp
 127 195 200 205
 128 Met Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro
 129 210 215 220
 130 Ala Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser
 131 225 230 235 240
 132 Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile
 133 245 250 255
 134 Val Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn
 135 260 265 270
 136 Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp
 137 275 280 285
 140 <210> SEQ ID NO: 5
 141 <211> LENGTH: 307
 142 <212> TYPE: PRT
 143 <213> ORGANISM: *Bacillus licheniformis*
 145 <400> SEQUENCE: 5
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 148 Leu Leu Phe Ser Cys Val Ala Leu Ala Gly Cys Ala Asn Asn Gln Thr
 149 20 25 30
 150 Asn Ala Ser Gln Pro Ala Glu Lys Asn Glu Lys Thr Glu Met Lys Asp
 151 35 40 45
 152 Asp Phe Ala Lys Leu Glu Gln Phe Asp Ala Lys Leu Gly Ile Phe
 153 50 55 60
 154 Ala Leu Asp Thr Gly Thr Asn Arg Thr Val Ala Tyr Arg Pro Asp Glu
 155 65 70 75 80
 156 Arg Phe Ala Phe Ala Ser Thr Ile Lys Ala Leu Thr Val Gly Val Leu
 157 85 90 95
 158 Leu Gln Gln Lys Ser Ile Glu Asp Leu Asn Gln Arg Ile Thr Tyr Thr
 159 100 105 110

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160 Arg Asp Asp Leu Val Asn Tyr Asn Pro Ile Thr Glu Lys His Val Asp
 161 115 120 125
 162 Thr Gly Met Thr Leu Lys Glu Leu Ala Asp Ala Ser Leu Arg Tyr Ser
 163 130 135 140
 164 Asp Asn Ala Ala Gln Asn Leu Ile Leu Lys Gln Ile Gly Gly Pro Glu
 165 145 150 155 160
 166 Ser Leu Lys Lys Glu Leu Arg Lys Ile Gly Asp Glu Val Thr Asn Pro
 167 165 170 175
 168 Glu Arg Phe Glu Pro Glu Leu Asn Glu Val Asn Pro Gly Glu Thr Gln
 169 180 185 190
 170 Asp Thr Ser Thr Ala Arg Ala Leu Val Thr Ser Leu Arg Ala Phe Ala
 171 195 200 205
 172 Leu Glu Asp Lys Leu Pro Ser Glu Lys Arg Glu Leu Leu Ile Asp Trp
 173 210 215 220
 174 Met Lys Arg Asn Thr Thr Gly Asp Ala Leu Ile Arg Ala Gly Val Pro
 175 225 230 235 240
 176 Asp Gly Trp Glu Val Ala Asp Lys Thr Gly Ala Ala Ser Tyr Gly Thr
 177 245 250 255
 178 Arg Asn Asp Ile Ala Ile Ile Trp Pro Pro Lys Gly Asp Pro Val Val
 179 260 265 270
 180 Leu Ala Val Leu Ser Ser Arg Asp Lys Lys Asp Ala Lys Tyr Asp Asp
 181 275 280 285
 182 Lys Leu Ile Ala Glu Ala Thr Lys Val Val Met Lys Ala Leu Asn Met
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 184 Asn Gly Lys
 185 305
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 189 <211> LENGTH: 325
 190 <212> TYPE: PRT
 191 <213> ORGANISM: Streptomyces cacaoi
 193 <400> SEQUENCE: 6
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 196 Leu Ala Leu Val Pro Leu Val Ala Cys Gly Gln Ala Ser Gly Ser Glu
 197 20 25 30
 198 Ser Gly Gln Gln Pro Gly Leu Gly Gly Cys Gly Thr Ser Ala His Gly
 199 35 40 45
 200 Ser Ala Asp Ala His Glu Lys Glu Phe Arg Ala Leu Glu Lys Lys Phe
 201 50 55 60
 202 Asp Ala His Pro Gly Val Tyr Ala Ile Asp Thr Arg Asp Gly Gln Glu
 203 65 70 75 80
 204 Ile Thr His Arg Ala Asp Glu Arg Phe Ala Tyr Gly Ser Thr Phe Lys
 205 85 90 95
 206 Ala Leu Gln Ala Gly Ala Ile Leu Ala Gln Val Leu Arg Asp Gly Arg
 207 100 105 110
 208 Glu Val Arg Arg Gly Ala Glu Ala Asp Gly Met Asp Lys Val Val His
 209 115 120 125
 210 Tyr Gly Gln Asp Ala Ile Leu Pro Asn Ser Pro Val Thr Glu Lys His
 211 130 135 140

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212 Val Ala Asp Gly Met Ser Leu Arg Glu Leu Cys Asp Ala Val Val Ala
 213 145 150 155 160
 214 Tyr Ser Asp Asn Thr Ala Ala Asn Leu Leu Phe Asp Gln Leu Gly Gly
 215 165 170 175
 216 Arg Arg Gly Ser Thr Arg Val Leu Lys Gln Leu Gly Asp His Thr Thr
 217 180 185 190
 218 Ser Met Asp Arg Tyr Glu Gln Glu Leu Gly Ser Ala Val Pro Gly Asp
 219 195 200 205
 220 Pro Arg Asp Thr Ser Thr Pro Arg Ala Phe Ala Glu Asp Leu Arg Ala
 221 210 215 220
 222 Phe Ala Val Glu Asp Gly Glu Lys Ala Ala Leu Ala Pro Asn Asp Arg
 223 225 230 235 240
 224 Glu Gln Leu Asn Asp Trp Met Ser Gly Ser Arg Thr Gly Asp Ala Leu
 225 245 250 255
 226 Ile Arg Ala Gly Val Pro Lys Asp Trp Lys Val Glu Asp Lys Ser Gly
 227 260 265 270
 228 Gln Val Lys Tyr Gly Thr Arg Asn Asp Ile Ala Val Val Arg Pro Pro
 229 275 280 285
 230 Gly Arg Ala Pro Ile Val Val Ser Val Met Ser His Gly Asp Thr Gln
 231 290 295 300
 232 Asp Ala Glu Pro His Asp Glu Leu Val Ala Glu Ala Gly Leu Val Val
 233 305 310 315 320
 234 Ala Asp Gly Leu Lys
 235 325
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 239 <211> LENGTH: 36
 240 <212> TYPE: DNA
 241 <213> ORGANISM: Artificial Sequence
 243 <220> FEATURE:
 244 <223> OTHER INFORMATION: synthetic primer
 246 <400> SEQUENCE: 7
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 250 <211> LENGTH: 30
 251 <212> TYPE: DNA
 252 <213> ORGANISM: Artificial Sequence
 254 <220> FEATURE:
 255 <223> OTHER INFORMATION: synthetic primer
 257 <400> SEQUENCE: 8
 258 tcgaaaatttt ttgttgtctt cctttttgg 30
 260 <210> SEQ ID NO: 9
 261 <211> LENGTH: 33
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 265 <220> FEATURE:
 266 <223> OTHER INFORMATION: synthetic primer
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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/589,233

DATE: 08/22/2006

TIME: 14:21:40

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L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date